Supplemental material for:

Metabolic modelling reveals broad changes in gut microbial metabolism in inflammatory bowel disease patients with dysbiosis

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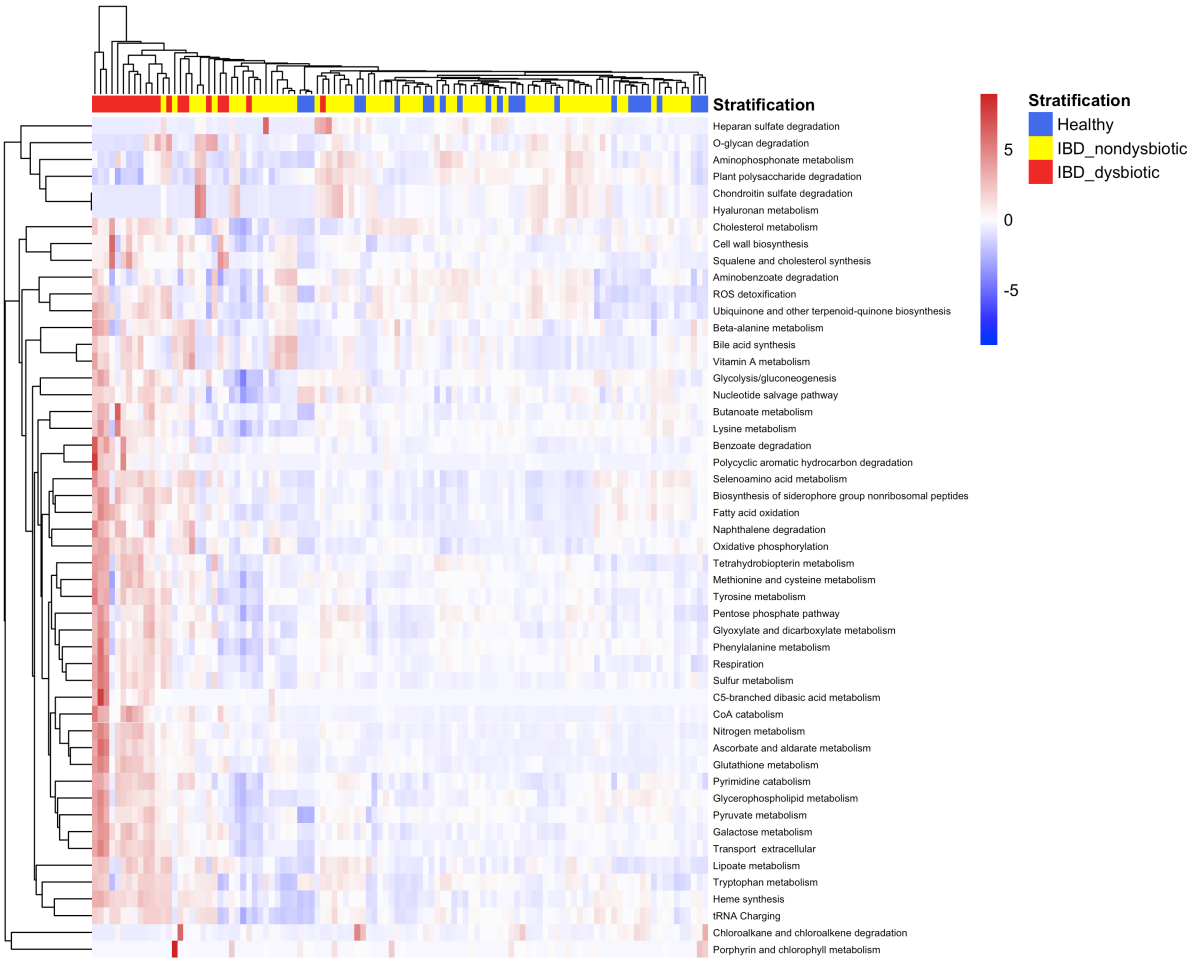
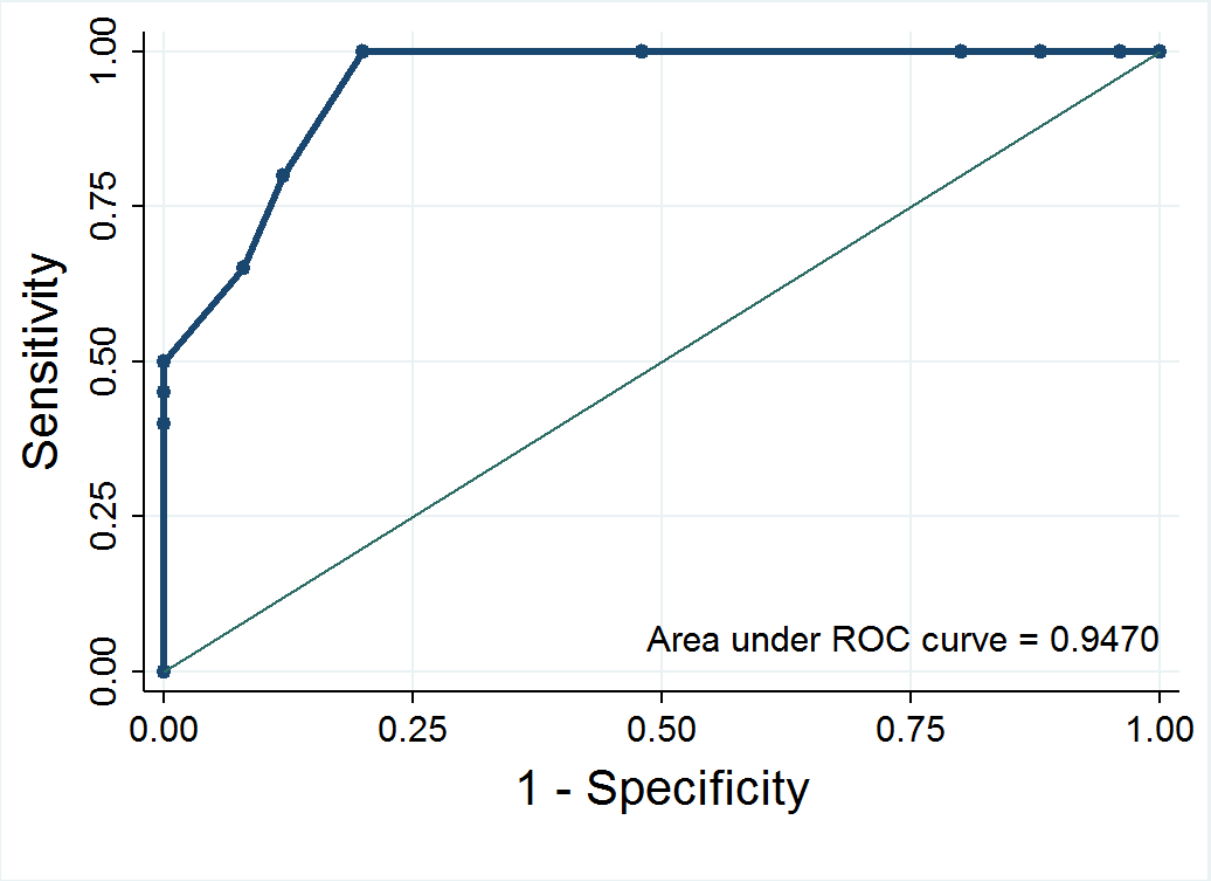
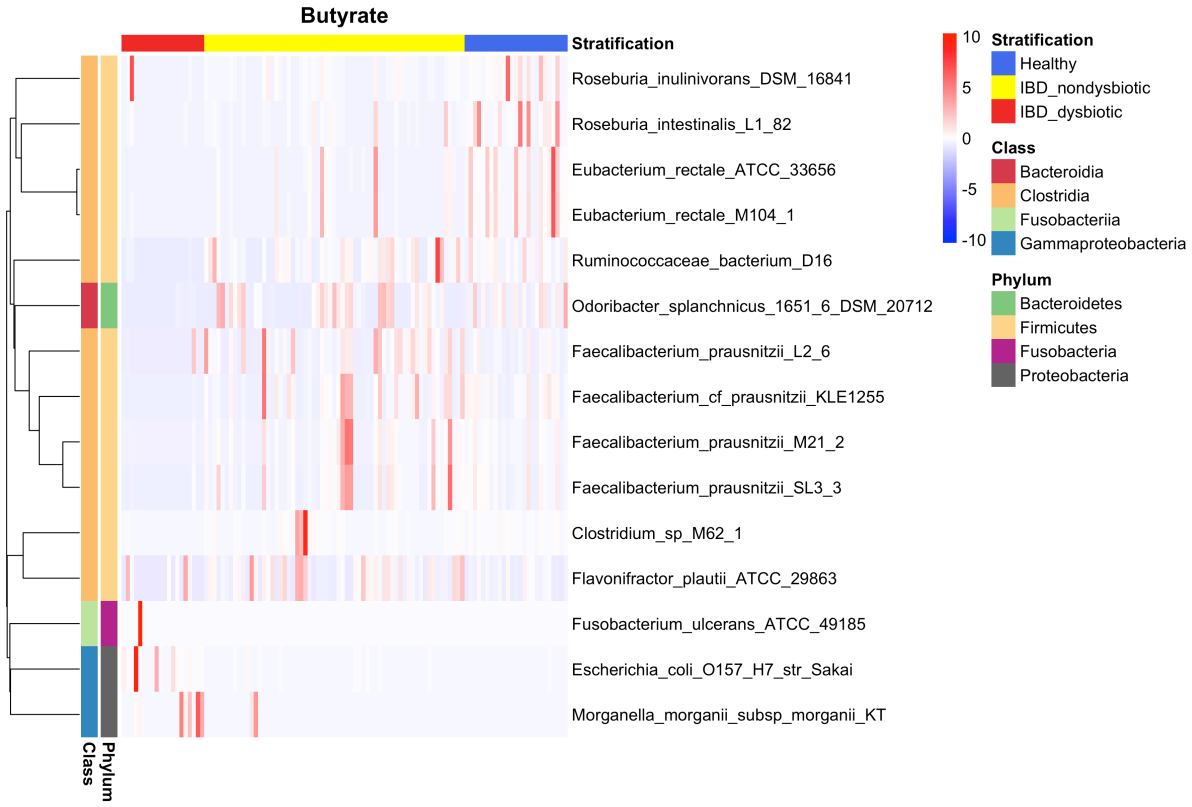


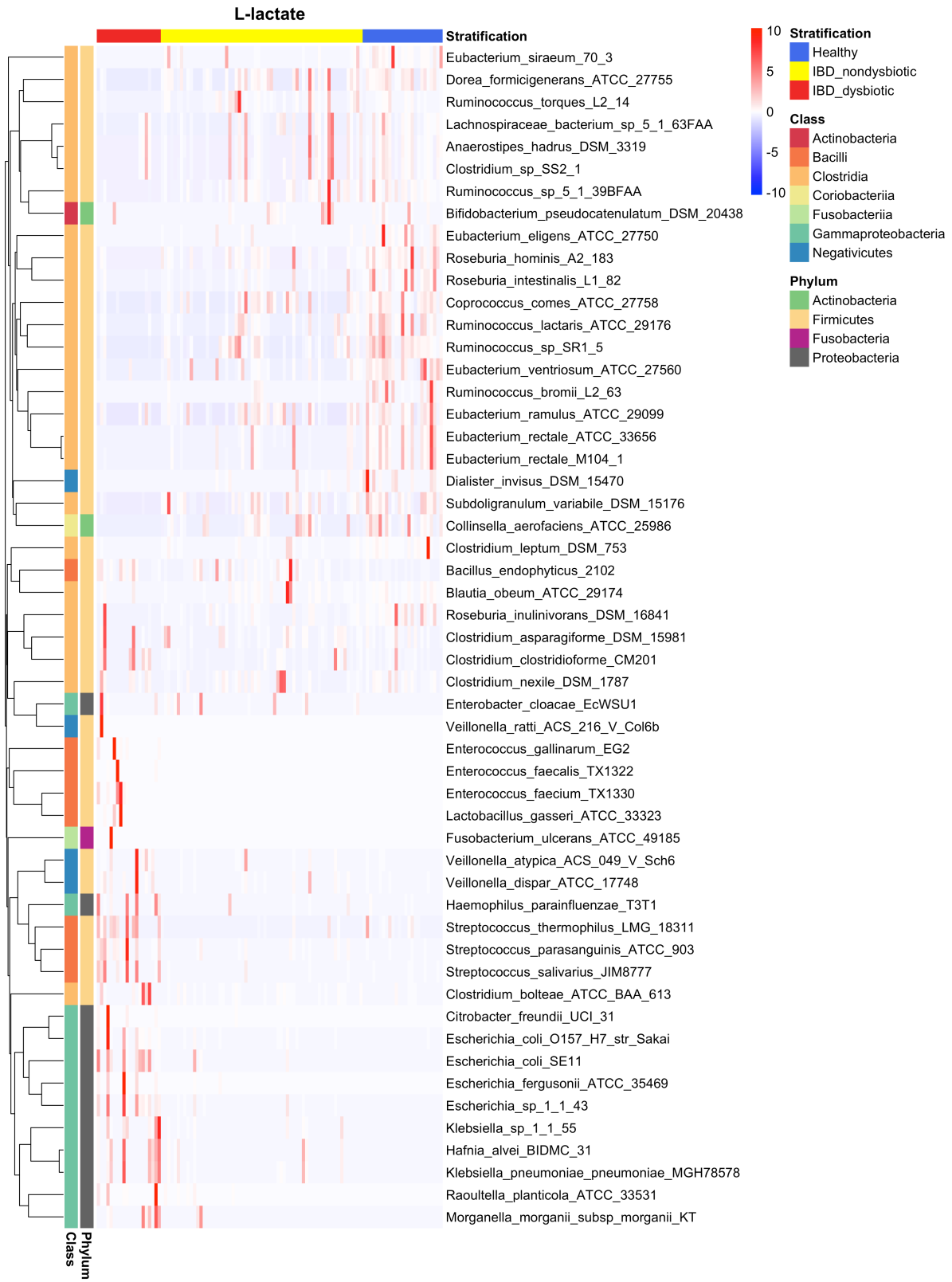
Supplementary Figure 1: Quantitative abundances of pathways in the 108 microbiomes. Shown are all subsystems that, after summarizing abundances for the corresponding reactions, were significantly different between healthy and IBD and/or between the dysbiotic and non-dysbiotic IBD cluster after correcting for false discovery rate.



Supplementary Figure 2: AUC from logistic regression, classifying healthy individuals using the number of independently secreted sulphur metabolites as only predictor. AUC is significantly bigger than 0.5, p=0.003.

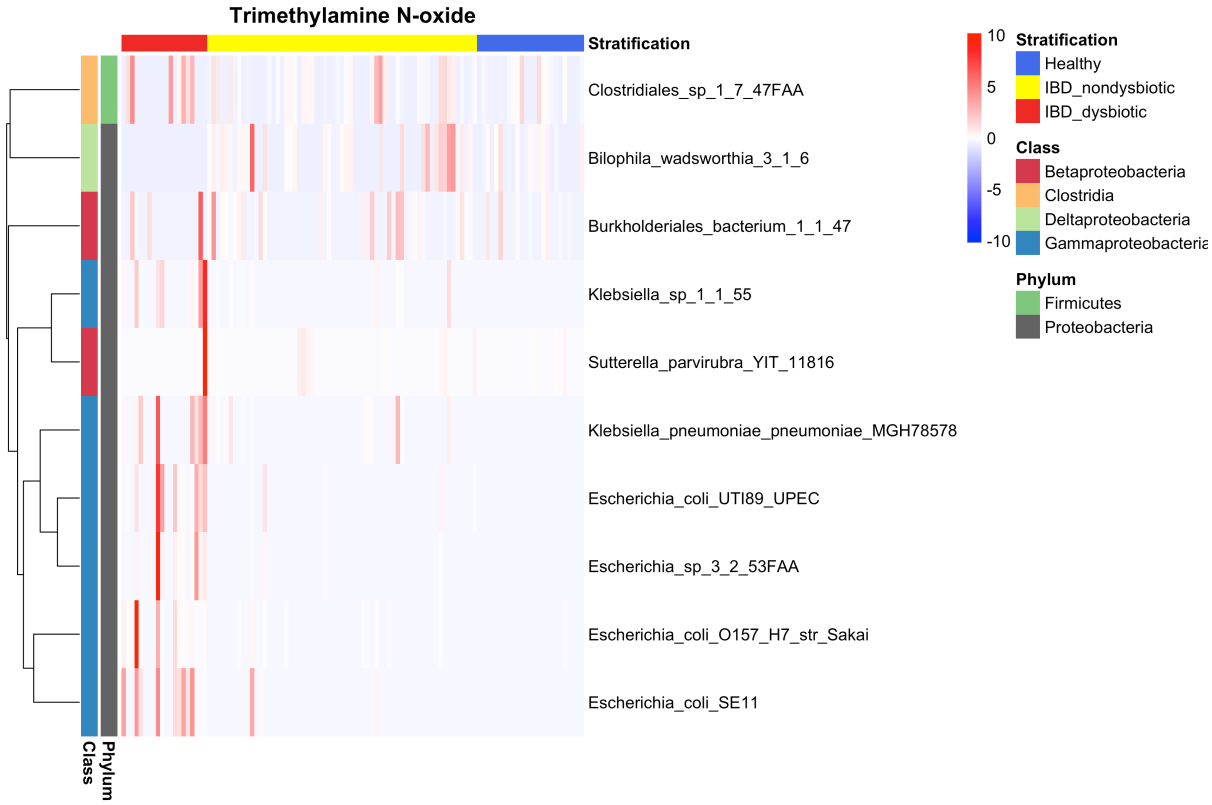


Supplementary Figure 3: Strain-level contributions to total butyrate production (mmol/person/day) in all 108 personalised microbiome models.

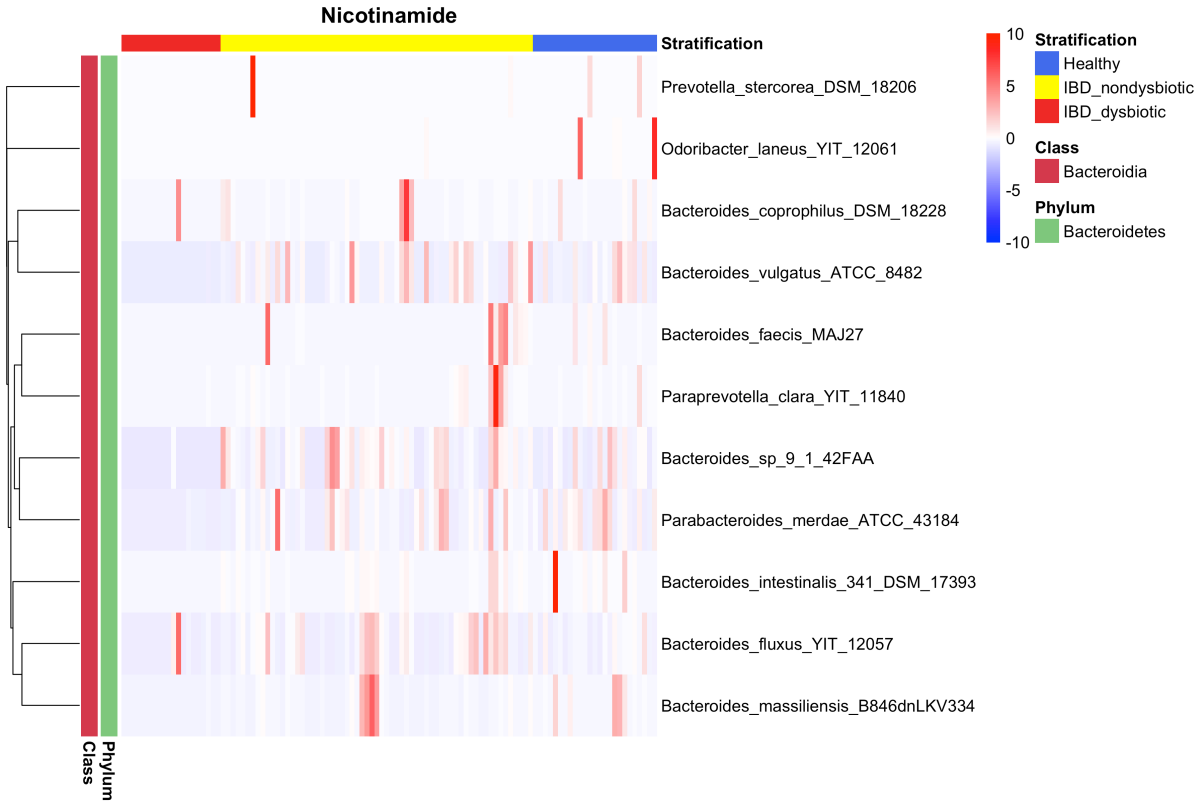


Supplementary Figure 4: Strain-level contributions to total L-lactate production (mmol/person/day) in all 108 personalised microbiome models.

Supplementary Figure 5: Strain-level contributions to total hydrogen sulphide production (mmol/person/day) in all 108 personalised microbiome models.

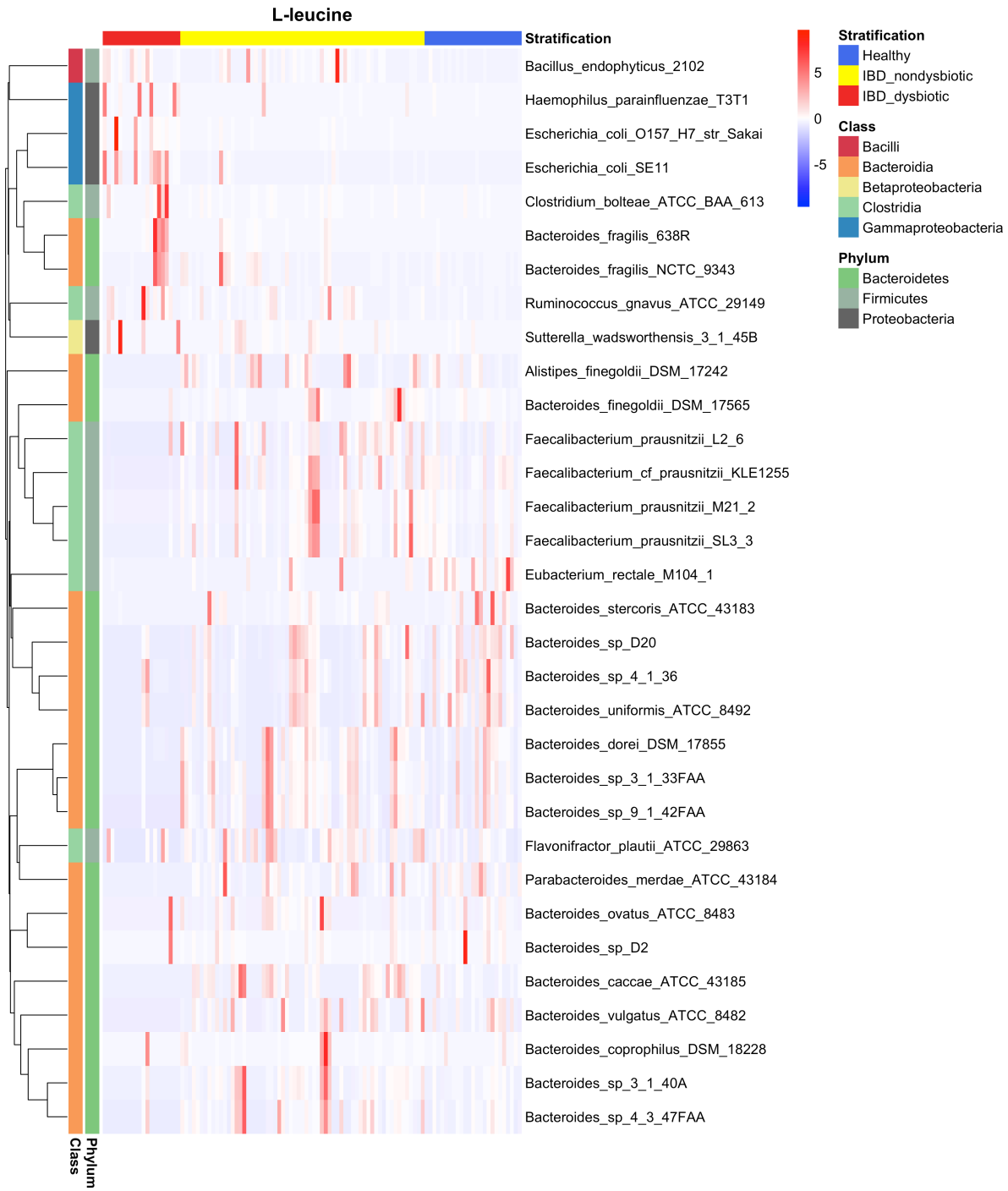


Supplementary Figure 6: Strain-level contributions to total trimethylamine-N-oxide production (mmol/person/day) in all 108 personalised microbiome models.



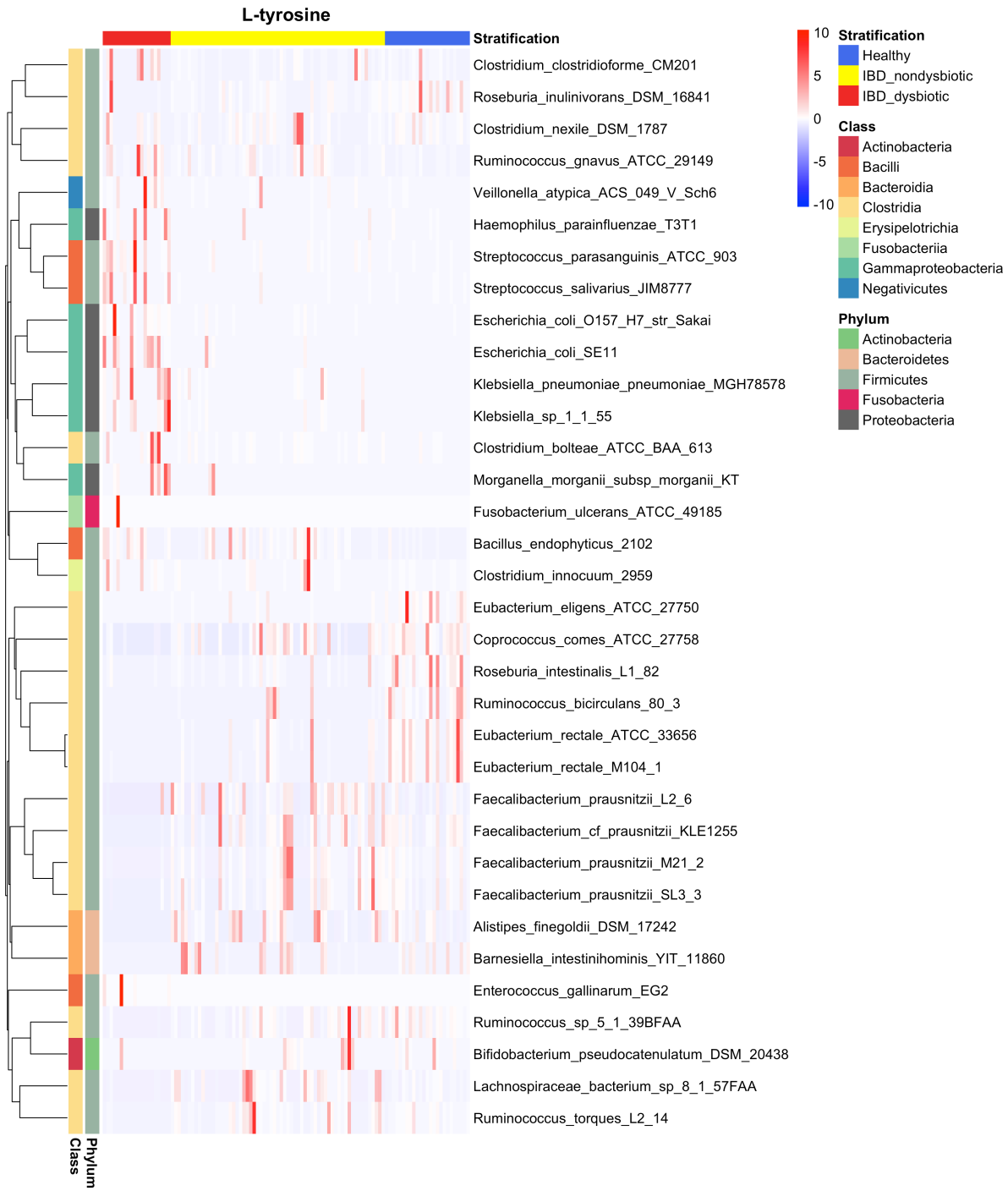
Supplementary Figure 7: Strain-level contributions to total nicotinamide production (mmol/person/day) in all 108 personalised microbiome models.

Supplementary Figure 8: Strain-level contributions to total glycine production (mmol/person/day) in all 108 personalised microbiome models.



Supplementary Figure 9: Strain-level contributions to total L-leucine production (mmol/person/day) in all 108 personalised microbiome models.

Supplementary Figure 10: Strain-level contributions to total L-phenylalanine production (mmol/person/day) in all 108 personalised microbiome models.



Supplementary Figure 11: Strain-level contributions to total L-tyrosine production (mmol/person/day) in all 108 personalised microbiome models.

Supplementary Figure 12: Strain-level contributions to total L-tryptophan production (mmol/person/day) in all 108 personalised microbiome models.